PATENT APPLICATION: US/09/777,317

DATE: 07/25/2001 TIME: 10:45:00

Input Set : N:\Crf3\RULE60\09777317.txt Output Set: N:\CRF3\07252001\1777317.raw

SEQUENCE LISTING

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2 (1) GENERAL INFORMATION:
             (i) APPLICANT: Gossen, Manfred
                             Bujard, Hermann
      4
      5
                             Salfeld, Jochen
      6
                             Voss, Jeffrey
      8
            (ii) TITLE OF INVENTION: Methods for Regulating Gene Expression
      9
           (iii) NUMBER OF SEQUENCES: 10
     10
            (iv) CORRESPONDENCE ADDRESS:
                   (A) ADDRESSEE: Lahive & Cockfield
     12
                   (B) STREET: 60 State Street, Suite 510
     13
     14
                   (C) CITY: Boston
     15
                   (D) STATE: Massachusetts
                  (E) COUNTRY: USA
     16
                   (F) ZIP: 02109-1875
     17
     18
             (V) COMPUTER READABLE FORM:
     19
                   (A) MEDIUM TYPE: Floppy disk
     20
                   (B) COMPUTER: IBM PC compatible
                   (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     21
                   (D) SOFTWARE: ASCII text
     22
     24
            (vi) CURRENT APPLICATION DATA:
                   (A) APPLICATION NUMBER: US/09/777,317
C--> 25
C--> 26
                  (B) FILING DATE: 25-Jul-2001
     27
                   (C) CLASSIFICATION:
           (vii) PRIOR APPLICATION DATA:
     31
     29
                   (A) APPLICATION NUMBER: 08/479,306
     30
                  (B) FILING DATE:
     32
                  (A) APPLICATION NUMBER: 08/076,327
     33
                  (B) FILING DATE: 14-JUN-1993
     34
          (viii) ATTORNEY/AGENT INFORMATION:
     35
                  (A) NAME: Giulio A. DeConti, Jr.
     36
                  (B) REGISTRATION NUMBER: 31,503
     37
                  (C) REFERENCE/DOCKET NUMBER: BBI-013CP3
            (ix) TELECOMMUNICATION INFORMATION:
     38
     39
                  (A) TELEPHONE: (617) 227-7400
     40
                  (B) TELEFAX: (617) 227-5941
     42
        (2) INFORMATION FOR SEQ ID NO: 1:
     44
             (i) SEQUENCE CHARACTERISTICS:
     45
                  (A) LENGTH: 1008 base pairs
     46
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
     47
     48
                  (D) TOPOLOGY: linear
     50
            (ii) MOLECULE TYPE: DNA (genomic)
     52
            (vi) ORIGINAL SOURCE:
     53
                  (A) ORGANISM: Herpes Simplex Virus
                  (B) STRAIN: K12, KOS
     54
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ENTERED

(vii) IMMEDIATE SOURCE:

56





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DATE: 07/25/2001 TIME: 10:45:00

Input Set : N:\Crf3\RULE60\09777317.txt Output Set: N:\CRF3\07252001\1777317.raw

57 (ix) FEATURE: 60 (A) NAME/KEY: exon 61 (B) LOCATION: 11008 63 (ix) FEATURE: 64 (A) NAME/KEY: mRNA 65 (B) LOCATION: 11008 67 (ix) FEATURE: 68 (A) NAME/KEY: misc. binding 69 (B) LOCATION: 1207 71 (ix) FEATURE: 72 (A) NAME/KEY: misc. binding 73 (B) LOCATION: 1207 71 (ix) FEATURE: 72 (A) NAME/KEY: misc. binding 73 (B) LOCATION: 208335 75 (ix) FEATURE: 76 (A) NAME/KEY: CDS 77 (B) LOCATION: 11005 78 (XI) SEQUENCE DESCRIPTION: SEQ ID NO: 1: 80 ATG TCT AGA TTA GAT AAA AGT AAA GTG ATT AAC AGC GCA TTA GAG CTG 81 Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu 82 1 5 10 15 84 CTT AAT GAG GTC GGA ATC GAA GGT TTA ACA ACC CGT AAA CTC GCC CAG 85 Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln 86 20 25 30 88 AAG CTA GGT GTA GAG CAG CCT ACA TTG TAT TGG CAT GTA AAA AAT AA 89 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys 90 35 40 45 91 CGG GCT TTG CTC GAC GCC TTA GAG GAG AGG ATT TTTA CGT AGA GAG AGG AAA AGG AGA AGA AGA AGA A	55 (D) (T) (T) (T)														
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65 (B) LOCATION: 1.1008 67 (IX) FEATURE: 68 (A) NAME/KEY: misc. binding 69 (B) LOCATION: 1207 71 (IX) FEATURE: 72 (A) NAME/KEY: misc. binding 73 (B) LOCATION: 208335 75 (IX) FEATURE: 76 (A) NAME/KEY: CDS 77 (B) LOCATION: 11005 79 (XI) SEQUENCE DESCRIPTION: SEQ ID NO: 1: 80 ATG TCT AGA TTA GAT AAA AGT AAA GTG ATT AAC AGC GCA TTA GAG CTG 81 Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu 82 1 1 5 10 15 84 CTT AAT GAG GAT GAA GGT TTA ACA ACC CGT AAA CTC GCC CAG 85 Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln 86 20 25 30 88 AAG CTA GGT GTA GAG CAC CTA CA TTG TAT TGG CAT GAA AAT AAC 89 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys 90 35 40 45 92 CGG GCT TTG CTC GAC GCC TTA GAC GAC ATT GAG CAC T192 93 Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His 94 50 55 60 96 ACT CAC TTT TGC CCT TTA GAA GGG GAA AGC TGC GAT GAC 97 Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg 98 65 70 75 80 100 AAT AAG GCT AAA AGT ACA GCG CCA GAA GAT TTT TTA CGT 97 Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg 98 65 70 75 80 100 AAT AAG GCT AAA AGT ATT AGA TAG CAC CAC AGA GAT TTT TTA CGT 98 ATG AAA GAC CAC TTT AGA CAC CAC ACA GAT TTT TTA CGT 98 ATG AAA GAC CAC TTT AGA CAC CAC ACA GAT TTT TTA CGT 98 ATT HIS PHE Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg 98 65 70 75 80 100 AAT AAG GCT AAA AGT TTT AGA CGC CAC ACA GAA AAC CAC CAT GAA AAC CAC CAT TO CAC ATT GAA CAC CAC CAC TTT TTA GAT AGA CAC CAC TTT TAGA CAC CAC TTT TAGA CAC CAC ACA GAT TTT AGA CAC CAC CAC ACA GAT AGA CAC CAC CAC CAC CAC CAC CAC CAC CAC															
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67 (ix) FEATURE: 68 (A) NAME/KEY: misc. binding 69 (B) LOCATION: 1207 71 (ix) FEATURE: 72 (A) NAME/KEY: misc. binding 73 (B) LOCATION: 208335 75 (ix) FEATURE: 76 (A) NAME/KEY: CDS 77 (B) LOCATION: 11005 79 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: 80 ATG TCT AGA TTA GAT AAA AGT AAA GTG ATT AAC AGC GCA TTA GAG CTG 81 Met Ser Arg Leu Asp Lys Ser Lys Val I1e Asn Ser Ala Leu Glu Leu 82 1 5 10 15 84 CTT AAT GAG GTC GGA ATC GAA GGT TTA ACA ACC CGT AAA CTC GCC CAG 85 Leu Asn Glu Val Gly I1e Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln 86 20 25 30 88 AAG CTA GGT GTA GAG CAG CCT ACA TG TAT TGG CAT GTA AAA AAT AAG 89 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys 90 35 40 45 91 GGG GCT TTG CTC GAC GCC TTA GAC ATG TAT GAT AGT AGT AGT AGT AGT AGT AGT	, ,														
68 (A) NAME/KEY: misc. binding 69 (B) LOCATION: 1207 71 (ix) FEATURE: 72 (A) NAME/KEY: misc. binding 73 (B) LOCATION: 208335 75 (ix) FEATURE: 76 (A) NAME/KEY: CDS 77 (B) LOCATION: 11005 77 (B) LOCATION: 11005 78 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: 80 ATG TCT AGA TTA GAT AAA AGT AAA GTG ATT ACA GC GCA TTA GAG CTG 81 Met Ser Arg Leu Asp Lys Ser Lys Val IIe Asn Ser Ala Leu Glu Leu 82 1 5 10 15 84 CTT AAT GAG GTC GGA ATC GAA GGT TTA ACA ACC CGT AAA CTC GCC CAG 85 Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln 86 20 25 30 88 AAG CTA GGT GTA GAG CAG CCT ACA TTG TAT TGG CAT GTA AAA AAT AAG 89 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys 90 35 40 45 92 CGG GCT TTG CTC GAC GCC TTA GCC ATT GAG ATG TATA GAG CAC CAT 92 ANG ALA Leu Leu Asp Ala Leu Ala IIe Glu Met Leu Asp Arg His His 94 50 50 60 96 ACT CAC TTT GC CCT TTA GAA GGG GAA AGC GGC CAA GAT TTT TTA CGT 97 Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg 98 65 70 75 80 100 AAT AAG GCT AAA AGT TTT AGA TGT CTTA CTA CGA CAG CAG CAG CAG 101 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly 102 85 90 95 104 GCA AAA GTA CAT TTA GGT ACA GG CCT ACA GAG AGA CAG CAT TTO TTA CAT 105 Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr 106 100 105 110 108 CTC GAA AAT CAA TTA GCC TT TTA TTA TTA TTA CGT CAG CAG CAT TTA GAT CAG CAG TTT TTA CAGT CAG CAG CAT TTO CTC ACA CAG CAG CAT TTT TTA CAGT CAG CAG CAG CAT TTT TA CAGT CAG	•														
1	67 (ix) FEATURE:														
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73	71 (ix) FEATURE:														
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79															
79	77 (B) LOCATION: 11005														
80 ATG TCT AGA TTA GAT AAA AGT AAA GTG ATA AAC AGC GCA TTA GAG CTG 81 Met Ser Arg Leu Asp Lys Ser Lys Val 11e Asn Ser Ala Leu Glu Leu 82 1 5 10 15 84 CTT AAT GAG GTC GGA ATC GAA GGT TTA ACA ACC CGT AAA CTC GCC CAG 96 85 Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln 86 20 25 30 88 AAG CTA GGT GTA GAG CAG CCT ACA TTG TAT TGG CAT GTA AAA AAT AAG 144 89 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys 90 35 40 45 92 CGG GCT TTG CTC GAC GCC TTA GCA ATG GTA AAA AAT AAG 144 89 Ays Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His 94 50 55 60 96 ACT CAC TTT TGC CTT TTA GAA GGG GAA AGC TGG CAA GAT TTT TTA CGT 240 97 Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg 80 100 AAT AAG GCT AAA AGT TTT AGA TGT GCT TTA CTA AGT CAT CGC GAT GGA 101 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly 102 85 90 95 104 GCA AAA GTA CAT TTA GGT ACA CGG CCT ACA GAC ACA GAT TTT TCA GAT AGG ACT 105 Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr 106 100 115 120 125 112 AAT GCA AAT CAA ATTA GCC TTT TTA TTA CGC CAA GAA AAA CAG TAT GAA ACT 138 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys 114 130 115 120 125 115 Asn Ala Leu Tyr Ala Leu Ser Ala CCG CT AAA GAA GAA AGG GAA ACA ACA 1480 117 Val Leu Glu Asp Gln His Gln Val Ala Lys Glu Glu Arg Glu Thr 118 145 150 150 160 120 CCT ACT ACT GAT GAT ATG AGT ATG AGT ATG GAA ATTA CGA ATG ACG CAT ATG ACA CGA CAA GCT ATT GAA ACG ACA ATTA CAT TTA AGG CAT CAA GAA GAA AGG GAA ACA ACA AGG CAT TTA CGC CAT CAA GAA AGG GAA ACA CAA AGG GAA ACA CAA AGG GAT CAA CAA GCT ATG GAG ACA CAA GCT TTT AGG CAA CAA GGT TTT AGG T GCC AGA CAA GCT GTT TTA GGT TGC CAT CAT GGG CAT TTT AGG T GCC GCT GTG GGG CAT TTT AGT TTA GGT TGC AGA CAA GCT GTT TTA GGT TGC CTT AGA GCT GTG GGG CAT TTT AGT TTA GGT TGC AGA CAA GCT GTG GGG CAT TTT AGT TTA GGT TGC AGA CAA GCT GTG GGG CAT TTT AGT TTA GGT TGC AGA CAA GCT GTG GGG CAT TTT AGT TTA GGT TGC AGA CAA GCT GTG G															
81 Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu 82 1 5 10 15 84 CTT AAT GAG GTC GGA ATC GAA GGT TTA ACA ACC CGT AAA CTC GCC CAG 96 85 Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln 86		48													
82															
84 CTT AAT GAG GTC GGA ATC GAA GGT TTA ACA ACC CGT AAA CTC GCC CAG 85 Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln 86															
85 Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln 86		96													
86		<i>- - - - - - - - - -</i>													
88 AAG CTA GGT GTA GAG CAG CAG CAG CAC ACA TTG TAT TGG CAT GTA AAA AAT AAG 144 89 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys 40 45 92 CGG GCT TTG CTC GAC GCC TTA GCC ATT GAG ATG TTA GAT AGG CAC CAT 192 93 Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His Follow 60 96 ACT CAC TTT TGC CCT TTA GAA GGG GAA AGC TGG CAA GAT TTT TTA CGT 240 97 Thr His Phe Cys Pro Leu Glu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg 80 98 65 70 70 75 80 75 100 AAT AAG GCT AAA AGT TTT AGA TGT GCT TTA CTA AGT CAT CGC GAT GGA 288 101 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly 95 104 GCA AAA GTA CAT TTA GGT ACA CGG CCT ACA GAA AAA CAG TAT GAA ACT 336 105 Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr 10 106 CTC GAA AAT CAA TTA GCC TTT TTA TTA TGC CAA CAA GGT TTT TCA CTA GAG 384 109 Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu 125 112 AAT GCA TTA TAT GCA CTC AGC GCT GTG GGG CAT TTT ACT TTA GGT TGC 432 113 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys 140 114 130 135 140 135 140 115 15 150 150 125 160 116 GTA TTG GAA GAT CAA GAG CAT CAA GAC CAT CAA GAA GAA AGG AA AGG GAA ACA </td <td></td> <td></td>															
19		111													
90		T 4 4													
92 CGG GCT TTG CTC GAC GCC TTA GCC ATT GAG ATG TTA GAT AGG CAC CAT 93 Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His 94 50 55 60 96 ACT CAC TTT TGC CCT TTA GAA GGG GAA AGC TGG CAA GAT TTT TTA CGT 97 Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg 98 65 70 75 80 100 AAT AAG GCT AAA AGT TTT AGA TGT GCT TTA CTA AGT CAT CGC GAT GGA 101 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Ser His Arg Asp Gly 102 85 90 95 104 GCA AAA GTA CAT TTA GGT ACA CGG CCT ACA GAA AAA CAG TAT GAA ACT 105 Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr 106 100 Lou Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu 110 115 120 125 112 AAT GCA TTA TAT GCA CTC AGC GCT GTG GGG CAT TTT ACT TTA GGT TGC 1432 140 140 150 113 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys 114 130 135 145 115 150 150 155 160 120 CCT ACT ACT GAA AGT AGT AGG CCG CCA TTA TTA CGA CAA GAA AGA GAA AGA GAA ACA 480 128 CGC ACT ACT ACT GAT AGT AGT CAA GAG CAA GAA GAA AGG GAA ACA 480 170 Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr 181 145 150 150 155 160	· · · · · · · · · · · · · · · · · · ·														
93 Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His 94 50 55 60 96 ACT CAC TTT TGC CCT TTA GAA GGG GAA AGC TGG CAA GAT TTT TTA CGT 240 97 Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg 98 65 70 75 80 100 AAT AAG GCT AAA AGT TTT AGA TGT GCT TTA CTA CAT CGC GAT GGA 288 101 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly 102 85 90 95 104 GCA AAA GTA CAT TTA GGT ACA CGG CCT ACA GAA AAA CAG TAT GAA ACT 336 105 Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr 106 100 100 105 110 108 CTC GAA AAT CAA TTA GCC TTT TTA TGC CAA CAA GGT TTT TCA CTA GAG 384 109 Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu 110 115 120 125 112 AAT GCA TTA TAT GCA CTC AGC GCT GTG GGG CAT TTT ACT TTA GGT TGC 432 113 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys 114 130 135 140 115 135 140 116 GTA TTG GAA GAT CAA GAG CAT CAA GTC GCT AAA GAA AGG GAA ACA AGG GAA ACA AGG TAT GAA ACA AGG TAT GAA ACA AGG TAT GAA AGG GAA ACA AGG TAT GAA GAA AGG GAA ACA AGG TAT GAA GAA AGG GAA ACA AGG TAT GAA GAA GAA GAA GAA GAA GAA GA		100													
94		192													
96 ACT CAC TTT TGC CCT TTA GAA GGG GAA AGC TGG CAA GAT TTT TTA CGT 97 Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg 98 65 70 75 80 100 AAT AAG GCT AAA AGT TTT AGA TGT GCT TTA CTA AGT CAT CGC GAT GGA 101 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly 102 85 90 95 104 GCA AAA GTA CAT TTA GGT ACA CGG CCT ACA GAA AAA CAG TAT GAA ACT 105 Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr 106 100 105 110 108 CTC GAA AAT CAA TTA GCC TTT TTA TGC CAA CAA GGT TTT TCA CTA GAG 109 Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu 110 115 120 125 112 AAT GCA TTA TAT GCA CTC AGC GCT GTG GGG CAT TTT ACT TTA GGT TGC 113 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys 114 130 135 140 116 GTA TTG GAA GAT CAA GAG CAT CAA GTC GCT AAA GAA GAA AGG GAA ACA 17 Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr 118 145 150 150 155 160 120 CCT ACT ACT GAT AGT GAT AGT ATG CCG CCA TTA TTA CGA CAA GCT ATC GAA TTA															
97 Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg 98 65 70 70 75 80 100 AAT AAG GCT AAA AGT TTT AGA TGT GCT TTA CTA AGT CAT CGC GAT GGA 288 101 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly 102 85 90 95 104 GCA AAA GTA CAT TTA GGT ACA CGG CCT ACA GAA AAA CAG TAT GAA ACT 336 105 Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr 106 100 100 105 110 108 CTC GAA AAT CAA TTA GCC TTT TTA TGC CAA CAA GGT TTT TCA CTA GAG 384 109 Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu 110 115 120 120 125 112 AAT GCA TTA TAT GCA CTC AGC GCT GTG GGG CAT TTT ACT TTA GGT TGC 432 113 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys 114 130 135 135 140 116 GTA TTG GAA GAT CAA GAG CAT CAA GTC GCT AAA GAA GAA AGG GAA ACA 480 117 Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr 118 145 150 150 155 160 120 CCT ACT ACT GAT AGT AGT AGT AGG CCG CCA TTA TTA CGA CAA GCT ATC GAA TTA 528		240													
98 65		240													
100 AAT AAG GCT AAA AGT TTT AGA TGT GCT TTA CTA AGT CAT CGC GAT GGA 101 ASN Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly 102															
101 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly 102															
102		288													
104 GCA AAA GTA CAT TTA GGT ACA CGG CCT ACA GAA AAA CAG TAT GAA ACT 105 Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr 106															
105 Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr 106															
106 100 105 110 108 CTC GAA AAT CAA TTA GCC TTT TTA TGC CAA CAA GGT TTT TCA CTA GAG 384 109 Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu 125 110 115 120 125 112 AAT GCA TTA TAT GCA CTC AGC GCT GTG GGG CAT TTT ACT TTA GGT TGC 432 113 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys 140 114 130 135 140 116 GTA TTG GAA GAT CAA GAG CAT CAA GTC GCT AAA GAA GAA AGG GAA ACA 480 117 Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr 150 120 155 160 120 155 160		336													
108 CTC GAA AAT CAA TTA GCC TTT TTA TGC CAA CAA GGT TTT TCA CTA GAG 109 Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu 110	105 Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr														
109 Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gln Gly Phe Ser Leu Glu 110 - 115 - 2 AGC GCT GTG GGG CAT TTT ACT TTA GGT TGC 432 111 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys 114 - 130 - 135 - 135 115 GTA TTG GAA GAT CAA GAG CAT CAA GTC GCT AAA GAA AGG GAA ACA 480 117 Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr 118 145 - 150 GAT ACT ACT ACT GAA TTA 528	106 100 105 110														
110		384													
112 AAT GCA TTA TAT GCA CTC AGC GCT GTG GGG CAT TTT ACT TTA GGT TGC 432 113 ASN Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys 114 130 135 135 140 116 GTA TTG GAA GAT CAA GAG CAT CAA GTC GCT AAA GAA GAA AGG GAA ACA 480 117 Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr 118 145 156 150 150 150 150 150 150 150 150 150 150	109 Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu														
113 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys 114	110 115 120 125														
114 130 135 140 116 GTA TTG GAA GAT CAA GAG CAT CAA GTC GCT AAA GAA GAA GAA AGG GAA ACA 480 117 Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr 118 118 145 150 155 160 120 CCT ACT ACT GAT AGT AGT ATG CCG CCA TTA TTA CGA CAA GCT ATC GAA TTA 528	112 AAT GCA TTA TAT GCA CTC AGC GCT GTG GGG CAT TTT ACT TTA GGT TGC	432													
116 GTA TTG GAA GAT CAA GAG CAT CAA GTC GCT AAA GAA AGG GAA ACA 480 117 Val Leu Glu Asp Glu His Gln Val Ala Lys Glu Arg Glu Thr 118 145 150 155 155 160 528 120 CCT ACT ACT GAT AGT ATG CCG CCA TTA TTA CGA CAA GCT ATC GAA TTA 528	113 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys														
117 Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr 118 145 150 155 160 120 CCT ACT ACT GAT AGT AGG CCG CCA TTA TTA CGA CAA GCT ATC GAA TTA 528	114 130 135 140														
117 Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr 118 145	116 GTA TTG GAA GAT CAA GAG CAT CAA GTC GCT AAA GAA GAA AGG GAA ACA	480													
118 145 150 155 160 120 CCT ACT ACT GAT AGT ATG CCG CCA TTA TTA CGA CAA GCT ATC GAA TTA 528															
120 CCT ACT ACT GAT AGT ATG CCG CCA TTA TTA CGA CAA GCT ATC GAA TTA 528															
		528													
121 Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Ard Gin Ala lie Gin Leu	121 Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu														

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Input Set : N:\Crf3\RULE60\09777317.txt
Output Set: N:\CRF3\07252001\1777317.raw

122					165					170					175		
	TTT	GAT	CAC	CAA		GCA	GAG	CCA	GCC		TTA	TTC	GGC	CTT		TTG	576
						Ala											
126				180	- 1				185					190			
128	ATC	ATA	TGC	GGA	TTA	GAA	AAA	CAA	CTT	AAA	TGT	GAA	AGT	GGG	TCC	GCG	624
						Glu											
130			195	-			-	200		-	-		205	•			
132	TAC	AGC	CGC	GCG	CGT	ACG	AAA	AAC	AAT	TAC	GGG	TCT	ACC	ATC	GAG	GGC	672
133	Tyr	Ser	Arg	Ala	Arg	Thr	Lys	Asn	Asn	Tyr	Gly	Ser	Thr	Ile	Glu	Gly	
134		210					215					220					
136	CTG	CTC	GAT	CTC	CCG	GAC	GAC	GAC	GCC	CCC	GAA	GAG	GCG	GGG	CTG	GCG	720
137	Leu	Leu	Asp	Leu	Pro	Asp	Asp	Asp	Ala	Pro	Glu	Glu	Ala	Gly	Leu	Ala	
138	225					230					235					240	
140	GCT	CCG	CGC	CTG	TCC	TTT	CTC	CCC	GCG	GGA	CAC	ACG	CGC	AGA	CTG	TCG	768
141	Ala	Pro	Arg	Leu	Ser	Phe	Leu	Pro	Ala	Gly	His	Thr	Arg	Arg	Leu	Ser	
142					245					250					255		
144	ACG	GCC	CCC	CCG	ACC	GAT	GTC	AGC	CTG	GGG	GAC	GAG	CTC	CAC	TTA	GAC	816
145	Thr	Ala	Pro	Pro	Thr	Asp	Val	Ser	Leu	Gly	Asp	Glu	Leu	His	Leu	Asp	
146				260					265					270			
148	GGC	GAG	GAC	GTG	GCG	ATG	GCG	CAT	GCC	GAC	GCG	CTA	GAC	GAT	TTC	GAT	864
149	Gly	Glu	Asp	Val	Ala	Met	Ala	His	Ala	Asp	Ala	Leu	Asp	Asp	Phe	Asp	
150			275					280					285				
						GAC											912
	Leu	_	Met	Leu	Gly	Asp	_	Asp	Ser	Pro	Gly		Gly	Phe	Thr	Pro	
154		290					295					300					
						TAC											960
		Asp	Ser	Ala	Pro	Tyr	Gly	Ala	Leu	Asp		Ala	Asp	Phe	Glu		
	305	~- ~				310					315					320	4000
						GAT										TAG	1008
	GLu	GIn	Met	Phe		Asp	Pro	Leu	GIY		Asp	Glu	Tyr	GLY	_		
162		TND		TON	325	ano.	TD 1	10 1	`	330					335		
	(2)					SEQ											
165		(1)		_		IARA(3.0							
166 167			•	•		H: 33 amir			acic	15							
168			•	•		OGY:											
169		/ii \	•	•		PE:											
170						ESCRI	-		SEO 1	נוט אול	1. 2.						
	Met					Lys							Δla	T.211	Glu	T.e.n	
172	1	DCI	1119	LCu	5	цу	OCI	цу	VUI	10	11511	DCI	niu	пси	15	пси	
		Asn	Glu	Va l	Glv	Ile	Glu	Glv	Len		Thr	Ara	Lvs	Leu	Ala	Gln	
175			Olu	20		110	014	4 - 1	25			9	_10	30		0111	
	Lvs	Leu	Glv		Glu	Gln	Pro	Thr		Tvr	Trp	His	Val		Asn	Lvs	
178	-1-		35					40		-1-			45	-15		_10	
	Arq	Ala		Leu	asp	Ala	Leu		Ile	Glu	Met	Leu		Ara	His	His	
181		50			- 1		55					60		,			
183	Thr	His	Phe	Cys	Pro	Leu	Glu	Gly	Glu	Ser	Trp	Gln	Asp	Phe	Leu	Arg	
184	65			-		70		•			75		-			80	
	Asn	Lys	Ala	Lys	Ser	Phe	Arg	Cys	Ala	Leu	Leu	Ser	His	Arg	Asp	Gly	

RAW SEQUENCE LISTING DATE: 07/25/2001 PATENT APPLICATION: US/09/777,317 TIME: 10:45:00

Input Set : N:\Crf3\RULE60\09777317.txt
Output Set: N:\CRF3\07252001\1777317.raw

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85
187
189 Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
                                    105
                100
192 Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
193
                                120
195 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
                            135
        130
                                                140
198 Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
                        150
                                            155
201 Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
202
                                        170
                    165
204 Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
               180
                                    185
207 Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala
208 195
                                200
210 Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly
                            215
213 Leu Leu Asp Leu Pro Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala
                        230
                                            235
216 Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser
                                        250
217
                    245
219 Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
                                    265
222 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
           275
                                280
225 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
                            295
228 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
                                            315
229 305
                       310
231 Glu Gln Met Phe Thr Asp Pro Leu Gly Ile Asp Glu Tyr Gly Gly
                                        330
                    325
235 (2) INFORMATION FOR SEQ ID NO: 3:
        (i) SEQUENCE CHARACTERISTICS:
236
237
              (A) LENGTH: 894 base pairs
238
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
239
240
              (D) TOPOLOGY: linear
242
        (ii) MOLECULE TYPE: DNA (genomic)
        (vi) ORIGINAL SOURCE:
244
              (A) ORGANISM: Herpes Simplex Virus
245
              (B) STRAIN: K12, KOS
246
              (C) INDIVIDUAL ISOLATE: tTAS transactivator
247
        (ix) FEATURE:
249
250
             (A) NAME/KEY: exon
251
             (B) LOCATION: 1..894
        (ix) FEATURE:
253
254
              (A) NAME/KEY: mRNA
              (B) LOCATION: 1..894
255
        (ix) FEATURE:
257
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DATE: 07/25/2001 TIME: 10:45:00

Input Set : N:\Crf3\RULE60\09777317.txt
Output Set: N:\CRF3\07252001\1777317.raw

	(A) NAME/KEY: misc. binding (B) LOCATION: 1207																
261																	
262																	
263																	
	(ix) FEATURE:																
266		(+11				KEY:	CDS										
267						ION:		891									
269		(xi							SEO	ID N	∩ · з						
		TCT											GCA	στια	GAG	СТС	48
		Ser															40
272	1		5		5	-1-		-10		10		001	III.u	LIC u	15	Lea	
		AAT	GAG	GTC		ATC	GAA	GGT	тта		ACC	CGT	AAA	СТС		CAG	96
		Asn															30
275				20	1			1	25			*** 5		30		OII.	
276	AAG	CTA	GGT		GAG	CAG	CCT	ACA		TAT	TGG	CAT	GTA	_	ААТ	AAG	144
		Leu															
278	•		35					40		-1-			45	-1-		_10	
279	CGG	GCT	TTG	CTC	GAC	GCC	TTA	GCC	ATT	GAG	ATG	TTA		AGG	CAC	CAT	192
		Ala															
281	•	50			-		55					60		,			
282	ACT	CAC	TTT	TGC	CCT	TTA	GAA	GGG	GAA	AGC	TGG	CAA	GAT	TTT	TTA	CGT	240
283		His															
284	65					70					75		_			80	
285	AAT	AAC	GCT	AAA	AGT	TTT	AGA	TGT	GCT	TTA	CTA	AGT	CAT	CGC	GAT	GGA	288
286	Asn	Asn	Ala	Lys	Ser	Phe	Arg	Cys	Ala	Leu	Leu	Ser	His	Arg	Asp	Gly	
287					85					90					95		
288	GCA	AAA	GTA	CAT	TTA	GGT	ACA	CGG	CCT	ACA	GAA	AAA	CAG	TAT	GAA	ACT	336
289	Ala	Lys	Val	His	Leu	Gly	Thr	Arg	Pro	Thr	Glu	Lys	Gln	Tyr	Glu	Thr	
290				100					105					110			
		GAA															384
	Leu	Glu		Gln	Leu	Ala	Phe	Leu	Cys	Gln	Gln	Gly	Phe	Ser	Leu	Glu	
293			115					120					125				
		GCA															432
	Asn	Ala	Leu	Tyr	Ala	Leu		Ala	Val	Gly	His		Thr	Leu	Gly	Cys	
296	am.	130	~		~		135					140					
		TTG															480
		Leu	Glu	Asp	Gin		His	Gln	Val	Ala		Glu	Glu	Arg	Glu		
	145	3 GM		a		150	~~~	~~-			155				_ 0	160	
		ACT															528
	Pro	Thr	Thr	Asp		мет	Pro	Pro	Leu		Arg	GIn	Ala	He		Leu	
302	m m m	CAM	CAC	(T A A	165	COA	C A C	003	000	170		mma	000	amm	175	mma	57 6
		GAT															576
304	rne	Asp	птВ		стλ	Ата	GTU	Pro		rne	ьeu	Pue	GTA		Glu	Leu	
	አ ጥ ፖ	א ייי א	TICC	180	עייים א	C A A	א א א	CAA	185	77 77 78	mcm	~ ~ ~	N CITT	190	mam	CIA m	604
		ATA															624
308	116	Ile	195	атХ	пеп	GIU	пур	200	ьeu	ьγѕ	Cys	GIU		στλ	ser	ASP	
	$CC\Delta$	TCG		CAC	A C C	CCC	λCλ		TICC	N.C.C	CCC	ccc	205	N C C	CAD	CTC	672
505	CCA	100	TIT	CAC	ACG	CGC	AUA	CIG	TCG	ACG	GCC		CCG	ACC	GAI	GIC	672

VERIFICATION SUMMARY

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L:25 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:] L:26 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

STATISTICS SUMMARY

PATENT APPLICATION: US/09/777,317

DATE: 07/25/2001

TIME: 10:45:01

Input Set : N:\Crf3\RULE60\09777317.txt
Output Set: N:\CRF3\07252001\1777317.raw

Application Serial Number: US/09/777,317

Alpha or Numeric: Alpha

Application Class:

Application File Date: 07-25-2001

Art Unit:

Software Application: Other Total Number of Sequences: 10 Total Nucleotides: 14449 Total Amino Acids: 632

Total Amino Acids: 632 Number of Errors: 0 Number of Warnings: 0 Number of Corrections: 1

MESSAGE SUMMARY

220 C: 1 (Keyword misspelled or invalid format)